

Response to Office Action of March 26, 2003
Application No. 09/83,264

AMENDMENTS TO THE CLAIMS

1. (currently amended) A method for screening for compounds that affect uncoupling, comprising:
- (a) contacting a mammalian cell or tissue sample with a candidate compound; and
 - (b) analyzing the expression of a polypeptide having at least 90% sequence identity to the polypeptide encoded by SEQ ID NO:1 or 2; and
analyzing mitochondrial membrane potential, and having uncoupling activity, within the sample

2-26. (canceled)

27. (currently amended) The method of Claim 1-claim 1, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 95% amino acid sequence identity to the protein encoded by SEQ ID NO:1 or 2.

28. (currently amended) The method of Claim 1-claim 1, wherein the mammalian cell or tissue sample is a human cell or tissue sample.

29. (currently amended) The method of Claim 1-claim 1, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 90% amino acid sequence identity to the protein encoded by SEQ ID NO:1.

30. (currently amended) The method of Claim 1-claim 1, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 90% amino acid sequence identity to the protein encoded by SEQ ID NO:2.

31. (currently amended) The method of Claim 1-claim 28, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 95% amino acid sequence identity to the protein encoded by SEQ ID NO:1 or 2.

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32. (currently amended) The method of Claim- claim 28, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 90% amino acid sequence identity to the protein encoded by SEQ ID NO:1.

33. (currently amended) The method of Claim- claim 28, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 90% amino acid sequence identity to the protein encoded by SEQ ID NO:2.

34. (currently amended) The method of Claim 1- claim 1, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 95% amino acid sequence identity to the protein encoded by SEQ ID NO:1.

35. (currently amended) The method of Claim 1- claim 1, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 95% amino acid sequence identity to the protein encoded by SEQ ID NO:2.

36. (currently amended) The method of Claim- claim 28, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 95% amino acid sequence identity to the protein encoded by SEQ ID NO:1.

37. (currently amended) The method of Claim- claim 28, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 95% amino acid sequence identity to the protein encoded by SEQ ID NO:2.

38. (new) The method of claim 1, wherein the candidate compound is a member selected from the group consisting of a small molecule, a polynucleotide, a modified polynucleotide, a polypeptide, an antibody, an antibody fragment and a modified antibody.

39. (new) The method of claim 1, wherein the polypeptide is SEQ ID NO:1.

40. (new) The method of claim 1, wherein the polypeptide is SEQ ID NO:2.

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41. (new) A method for screening for compounds that affect uncoupling, comprising:

contacting a mammalian cell or tissue sample with a candidate compound; analyzing expression of a polypeptide encoded by SEQ ID NO:1 or 2, and having uncoupling activity within the sample.

42. (new) The method of claim 41, wherein uncoupling activity is detecting the expression of the polypeptide.

43. (new) The method of claim 41, further comprising analyzing mitochondrial membrane potential in the sample.

44. (new) A method for screening for compounds that affect uncoupling, comprising:

contacting a mammalian cell or tissue sample with a candidate compound suspected of affecting uncoupling; and
analyzing expression of a polypeptide having at least 90% sequence identity to a polypeptide encoded by SEQ ID NO:1 or 2.

45. (new) The method of claim 44, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 95% amino acid sequence identity to the protein encoded by SEQ ID NO:1 or 2.

46. (new) The method of claim 44, wherein the mammalian cell or tissue sample is a human cell or tissue sample.

47. (new) The method of claim 44, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 90% amino acid sequence identity to the protein encoded by SEQ ID NO:1.

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48. (new) The method of claim 44, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 90% amino acid sequence identity to the protein encoded by SEQ ID NO:2.

49. (new) The method of claim 46, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 95% amino acid sequence identity to the protein encoded by SEQ ID NO:1 or 2.

50. (new) The method of claim 46, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 90% amino acid sequence identity to the protein encoded by SEQ ID NO:1.

51. (new) The method of claim 46, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 90% amino acid sequence identity to the protein encoded by SEQ ID NO:2.

52. (new) The method of claim 44, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 95% amino acid sequence identity to the protein encoded by SEQ ID NO:1.

53. (new) The method of claim 44, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 95% amino acid sequence identity to the protein encoded by SEQ ID NO:2.

54. (new) The method of claim 46, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 95% amino acid sequence identity to the protein encoded by SEQ ID NO:1.

55. (new) The method of claim 46, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 95% amino acid sequence identity to the protein encoded by SEQ ID NO:2.

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56. (new) The method of claim 44, wherein the candidate compound is a member selected from the group consisting of a small molecule, a polynucleotide, a modified polynucleotide, a polypeptide, an antibody, an antibody fragment and a modified antibody.

57. (new) The method of claim 44, wherein the polypeptide is SEQ ID NO:1.

58. (new) The method of claim 44, wherein the polypeptide is SEQ ID NO:2.

59. (new) A method for screening for compounds that affect uncoupling, comprising:

contacting a mammalian cell or tissue sample with a candidate compound;
analyzing expression of a polypeptide having at least 90% sequence identity to a polypeptide encoded by SEQ ID NO:1 or 2; and
analyzing effect of the compound on membrane potential.

60. (new) The method of claim 59, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 95% amino acid sequence identity to the protein encoded by SEQ ID NO:1 or 2.

61. (new) The method of claim 59, wherein the mammalian cell or tissue sample is a human cell or tissue sample.

62. (new) The method of claim 59, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 90% amino acid sequence identity to the protein encoded by SEQ ID NO:1.

63. (new) The method of claim 59, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 90% amino acid sequence identity to the protein encoded by SEQ ID NO:2.

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14. (new) The method of claim 61, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 95% amino acid sequence identity to the protein encoded by SEQ ID NO:1 or 2.

15. (new) The method of claim 61, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 90% amino acid sequence identity to the protein encoded by SEQ ID NO:1.

16. (new) The method of claim 61, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 90% amino acid sequence identity to the protein encoded by SEQ ID NO:2.

17. (new) The method of claim 59, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 95% amino acid sequence identity to the protein encoded by SEQ ID NO:1.

18. (new) The method of claim 59, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 95% amino acid sequence identity to the protein encoded by SEQ ID NO:2.

19. (new) The method of claim 61, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 95% amino acid sequence identity to the protein encoded by SEQ ID NO:1.

20. (new) The method of claim 61, wherein the analyzing comprises analyzing the expression of a polypeptide having at least 95% amino acid sequence identity to the protein encoded by SEQ ID NO:2.

21. (new) The method of claim 59, wherein the candidate compound is a member selected from the group consisting of a small molecule, a polynucleotide, a modified polynucleotide, a polypeptide, an antibody, an antibody fragment and a modified antibody.

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72. (new) The method of claim 59, wherein the polypeptide is SEQ ID NO:1.

73. (new) The method of claim 59, wherein the polypeptide is SEQ ID NO:2.